

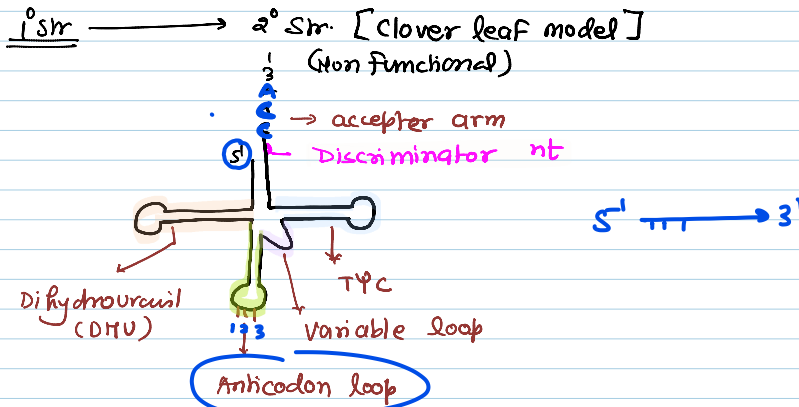
Translation

→ mRNA ✓

✓ → tRNA

→ Ribosome

tRNA →



Post Transcriptional modification

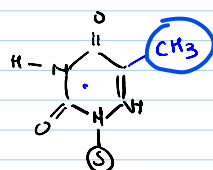
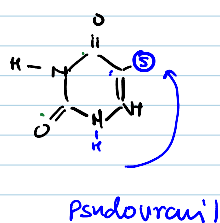
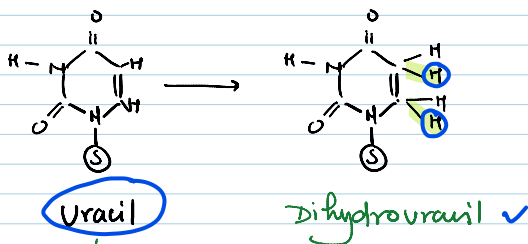
✓ [A] → N⁷-methyl adenine

[G] → O⁶ methyl Guanine

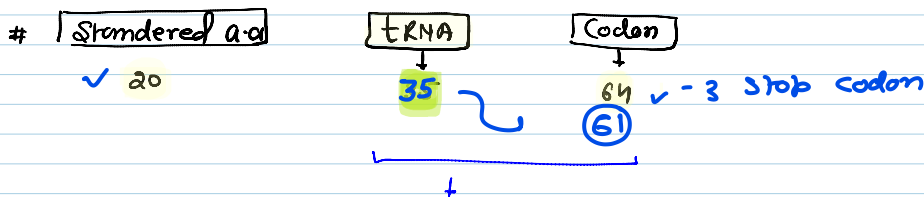
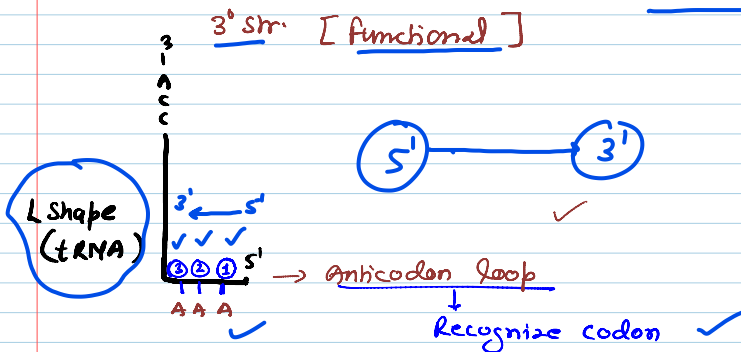
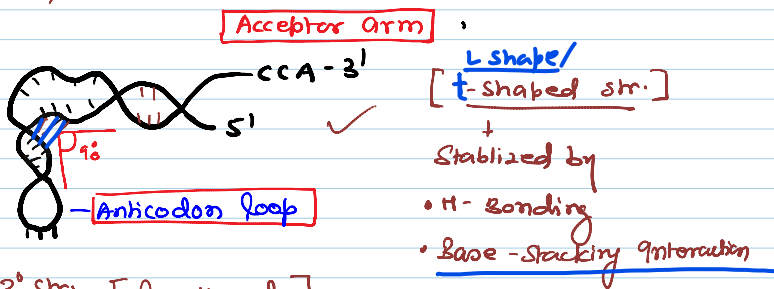
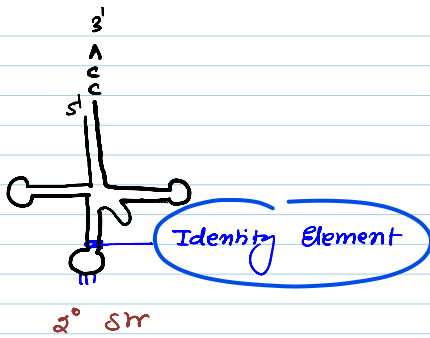
[C] → 5-methyl Cytosine

[U] → 5-methyl uracil

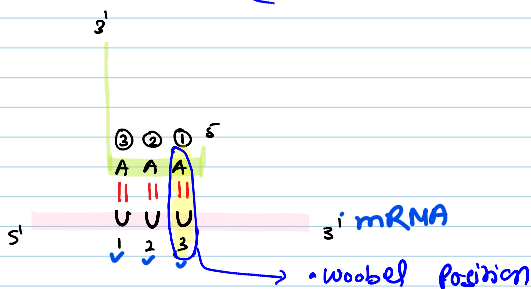
↳ Pseudouracil ✓
↳ Dihydrouracil ✓



= Thymine



- tRNA can recognize more Than one codon
- Reason → Wobbel position is tnt in 1st position of tRNA & 3rd position of codon (Anticodon)



- Flexibility is allowed
- Extended H-bonding can be

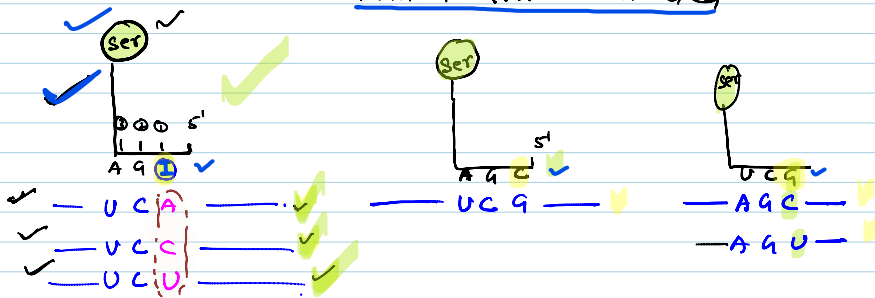
Seen

eq-

1 st position 5' Anticodon	3' codon-3 rd position
<p>A</p> <p>G</p> <p>C</p> <p>I (Inosine)</p>	<p>U</p> <p>C, U</p> <p>A</p> <p>A, C, U</p>

eq- Ser - has 6- codon

- more than 1 tRNA is needed



Iso acceptor tRNA

Different tRNA can accept same amino acid

Amino acid with 1 codon - one tRNA

a.a n 2 codon - 1 tRNA

a.a n 3 codon - 1 tRNA

a.a n 4 codon - 2 tRNA

& diff. tRNA that carry same a.a.

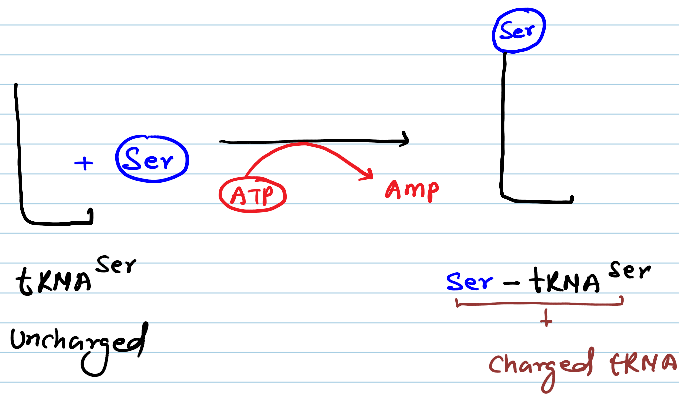
In mitochondria (Yeast & mammalian)

- only 20 tRNA + nt

→ more flexibility allowed than wobble flexibility

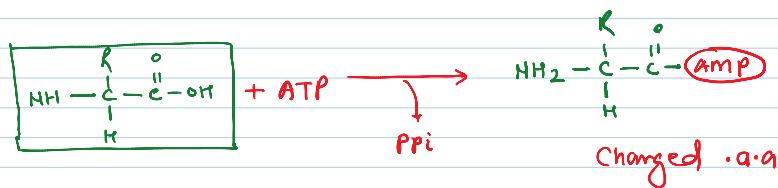
Plant mt → complete 35 tRNA present

loading of amino acid on tRNA -

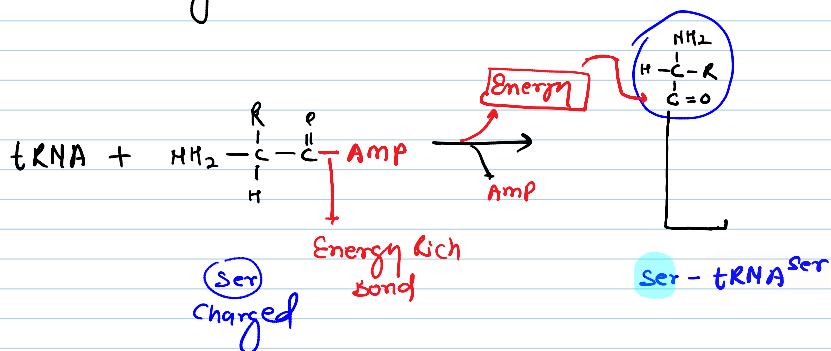


20 different a.a. tRNA Synthetase tnt to load 20 different a.a. on its tRNA

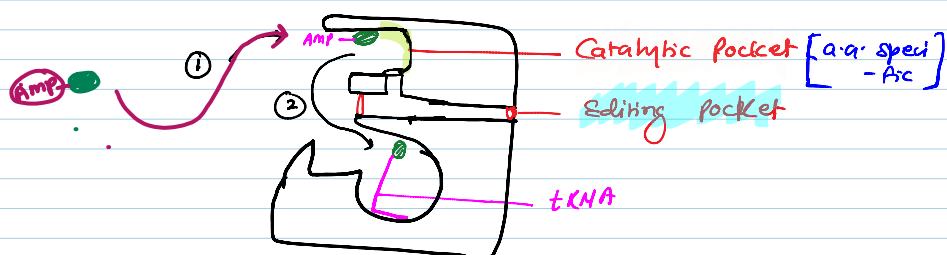
1st Step → Charging of a.a.



2nd Step - loading of charged a.a. on Acceptor arm of tRNA



tRNA Synthetase Catalyze This Rxn



a.a. loaded on tRNA

tRNA Synthetase add a.a. on 3' OH or 2' OH
of Acceptor Arm of tRNA

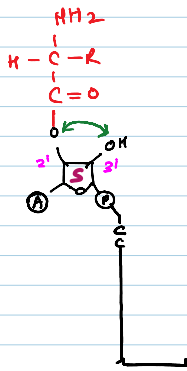
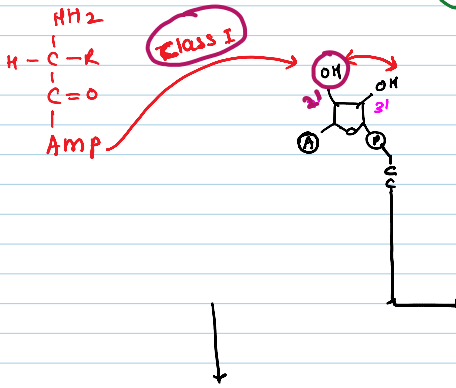
tRNA Synthetase

Class I

- Single Subunit ✓
- add a.a. on 2' OH
- ≈ 10 diff. Enzyme

Class II

- Dimer / Tetramer ✓
Enzyme
- add a.a. on 3' OH
- ≈ 10 diff. Enzyme



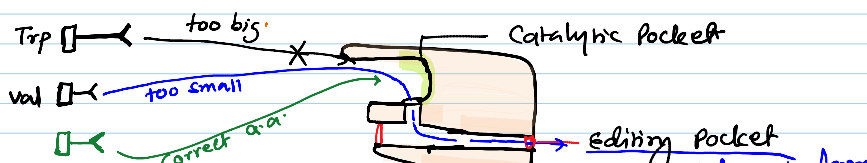
a.a. Can Suffer from 2' to 3' or from 3' to 2' OH

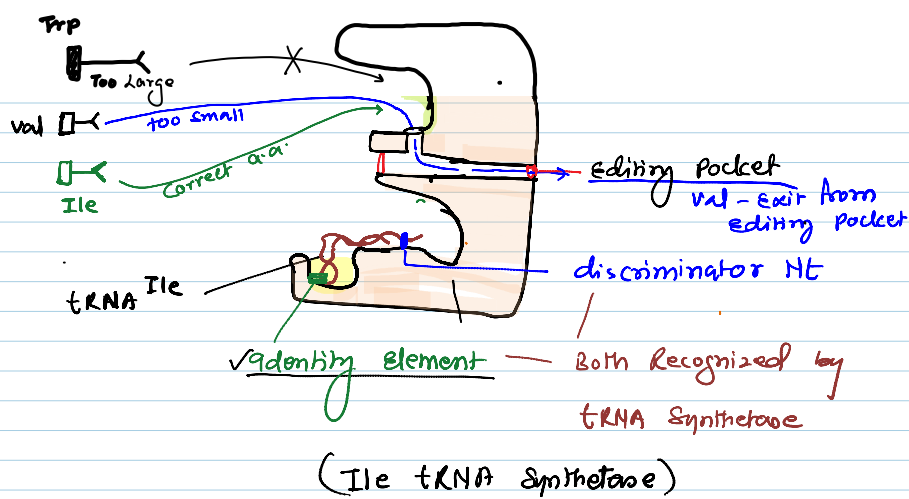
But after adding to specific 2' OH by Class I a.a. tRNA Synthetase

tRNA Contain —

- Identity Element → nt in Anticodon loop ✓
- Discriminator nt → nt in Acceptor arm

Helps in Recognition of Correct tRNA in active site of tRNA Synthetase

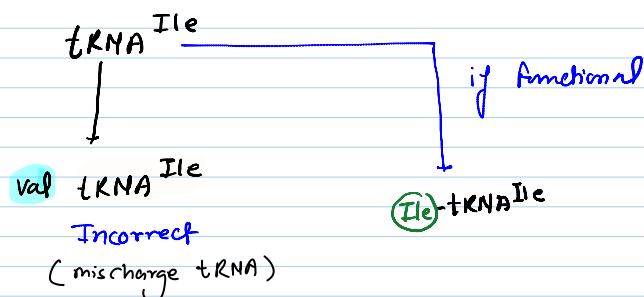




- ① Catalytic pocket → 1st proof reading step
- only respective a.a. can enter & fit into catalytic pocket
 - ✓ too large a.a. → can not enter
 - too small → enters into editing pocket

- ② Editing pocket
- ↳ wrong a.a. (small sized)
 - ↓
 - Exit from editing pocket ✓

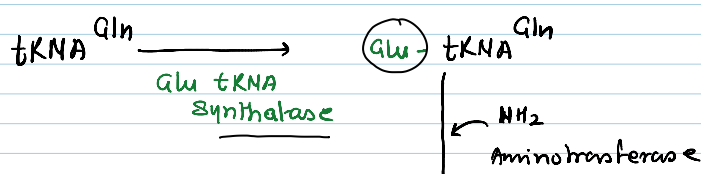
if editing pocket is non functional

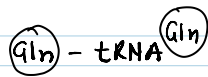


Error Rate - of tRNA Synthetase

- ✓ • Catalytic pocket - 1/100
 - ✓ • Editing pocket - 1/100
- 1/10000 a.a.

In some bacteria





• Selenocysteine → No tRNA Synthetase

Sec

a.a. + tnt in

- Glutathione peroxidase ✓
- formate Dehydrogenase ✓

tRNA^{Sec}

Recognized by
Ser tRNA Synthetase

Ser - tRNA^{Sec}

modifier
Enzyme

Selenium
O

Sec - tRNA^{Sec}

Note

Codon for Sec.
is UGA

Generally act as
Stop codon

But some times it act as
codon for Sec.

if tRNA^{Ile} is misCharged with val = val - tRNA^{Ile}

all the Ile site in protein
is replaced by val

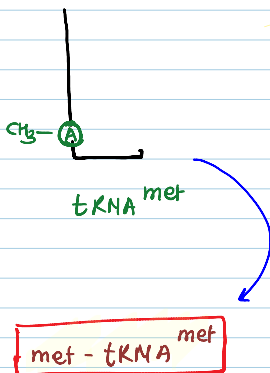
Initiator tRNA

Eukaryote

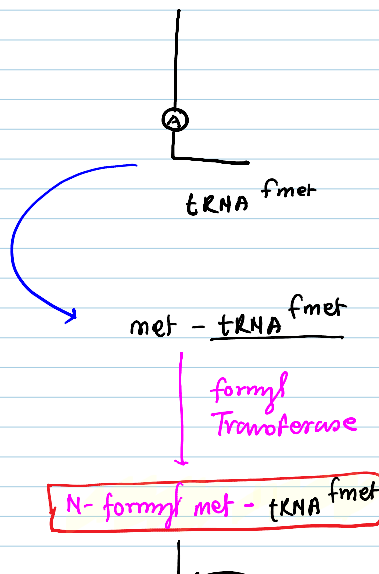
met - tRNA^{met}

Prokaryote

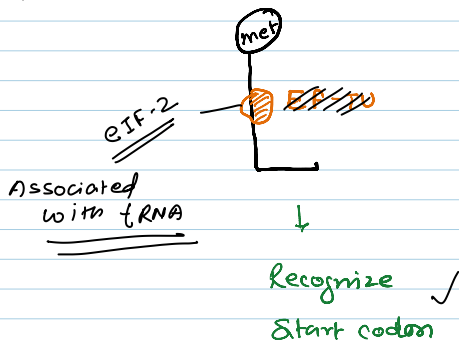
fmet - tRNA^{fmet}



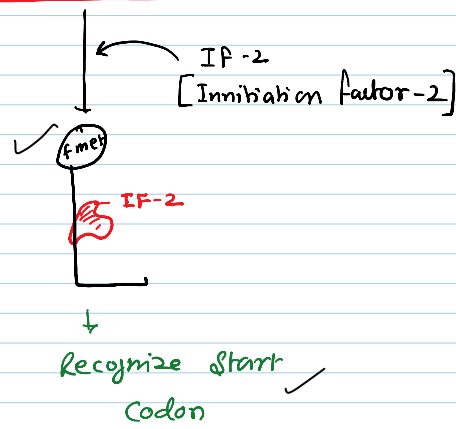
~~EF-Tu~~
~~Elongation Factor~~
~~Thermo unstable~~



[Elongation Factor]
[Thermo/ unstable]



N-formyl met - tRNA fmet



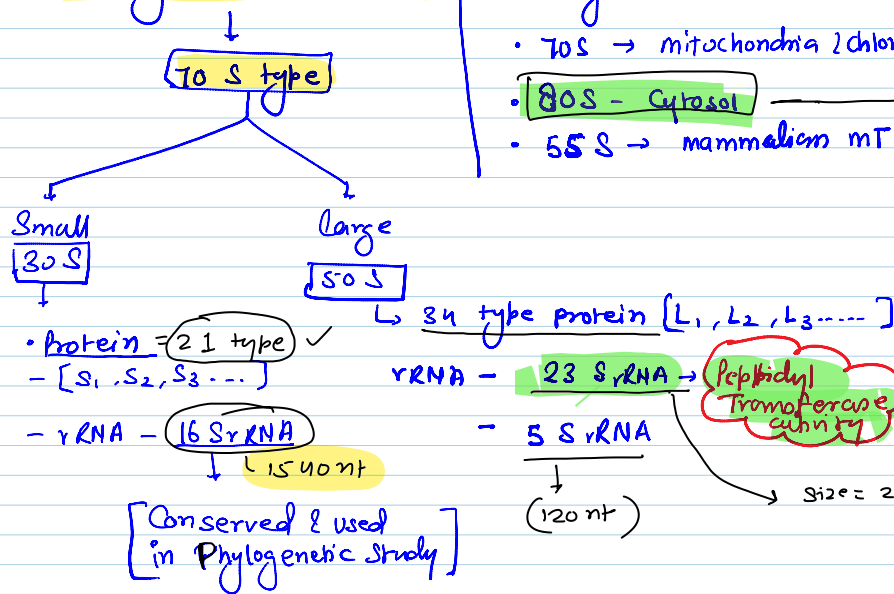
Translation

- mRNA ✓
- tRNA ✓
- Ribosome

Ribosome

- Assembly of tRNA & protein [Ribonucleo-protein]
- lack membrane

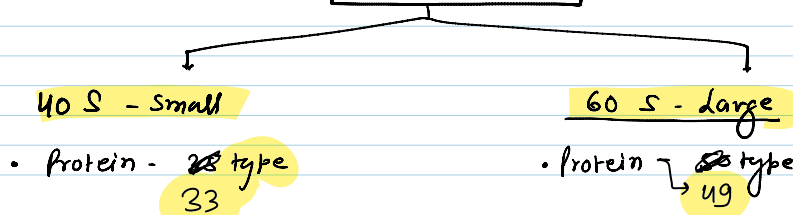
Prokaryotic Ribosome



Eukaryotic Ribosome

- 70S → mitochondria / chloroplast
 - 80S - Cytosol
 - 55S → mammalian mt
- 80S
- 60S
- 5.8S rRNA
5S rRNA
20S rRNA
+ 16 protein
- 40S
- 18S rRNA
+ 33 protein

80S Ribosome

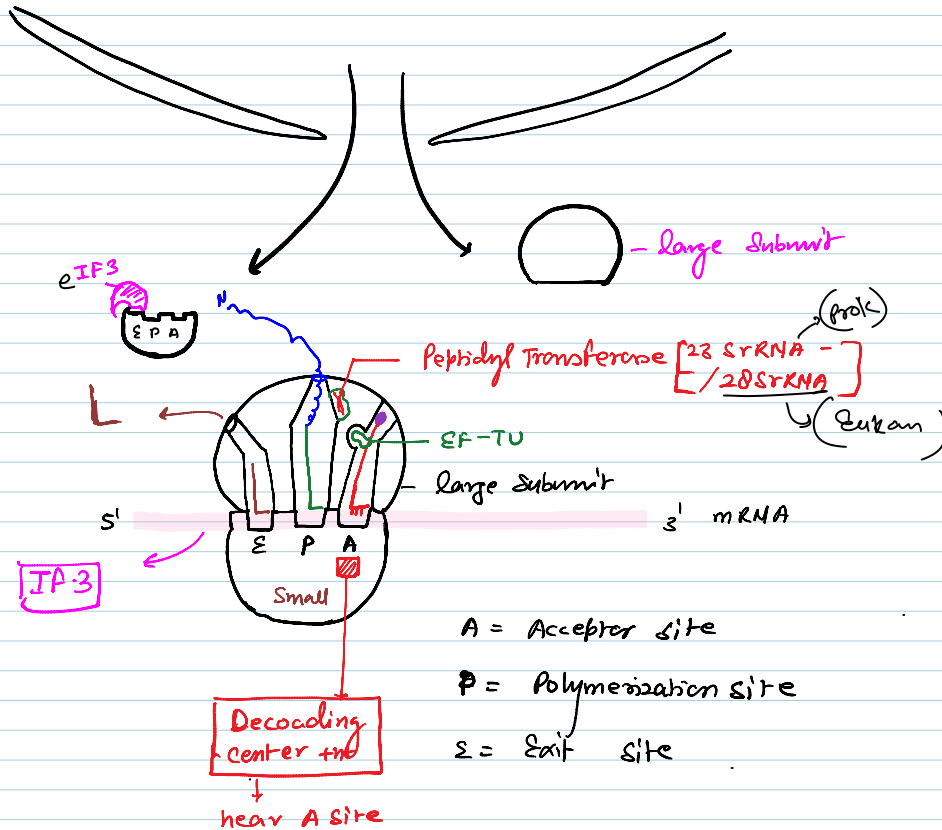


40 S - small

- Protein - 23 type
- rRNA - 18 S rRNA

60 S - large

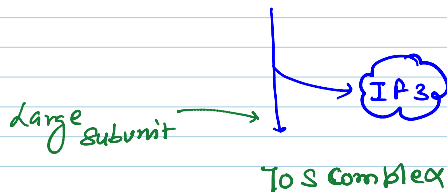
- Protein - 23 type
 - rRNA - 23 S
- 5.8 S
5.8 S rRNA
- Nucleolus



Translation in Prokaryote -

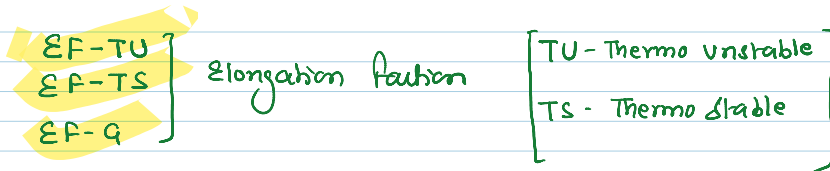
✓ ① Initiation

- 30S subunit of ribosome (small subunit)
- + Associated factor [IF-1, IF-2, IF-3]



② Elongation

- Peptide synthesis [at P site]



③ Termination

→ Release of peptide chain

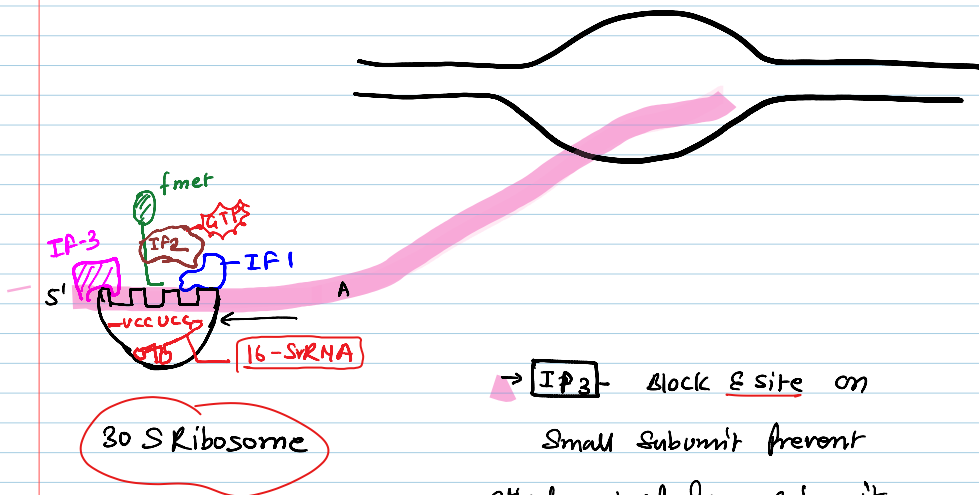
Release factor -

- ✓ - Class I R.P. → RF-1/RF-2
- ✓ - Class II R.P. → RF-3

④ Ribosome Release

- IF-3 ✓
- EF-G ✓
- Ribosome Release Factor [RRF]

Initiation in prokaryote -

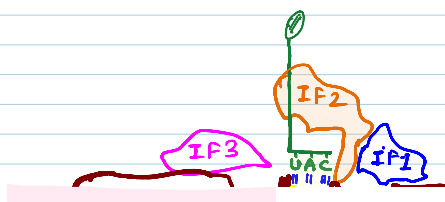


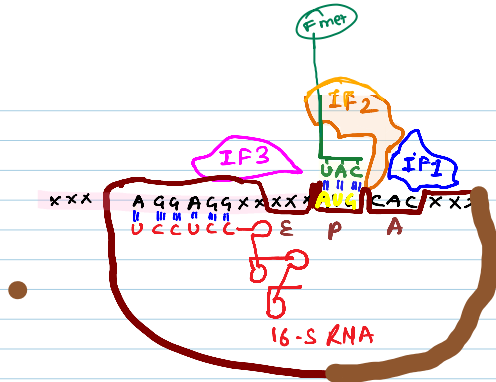
→ **IF-3** - Block E site on Small subunit prevent attachment of large subunit

→ **IF-2-GTP** → Interacts with —

- ✓ • tRNA on P-site
- ✓ • Small subunit of Ribosome
- ✓ • IF-1

IF-1 → Block A site

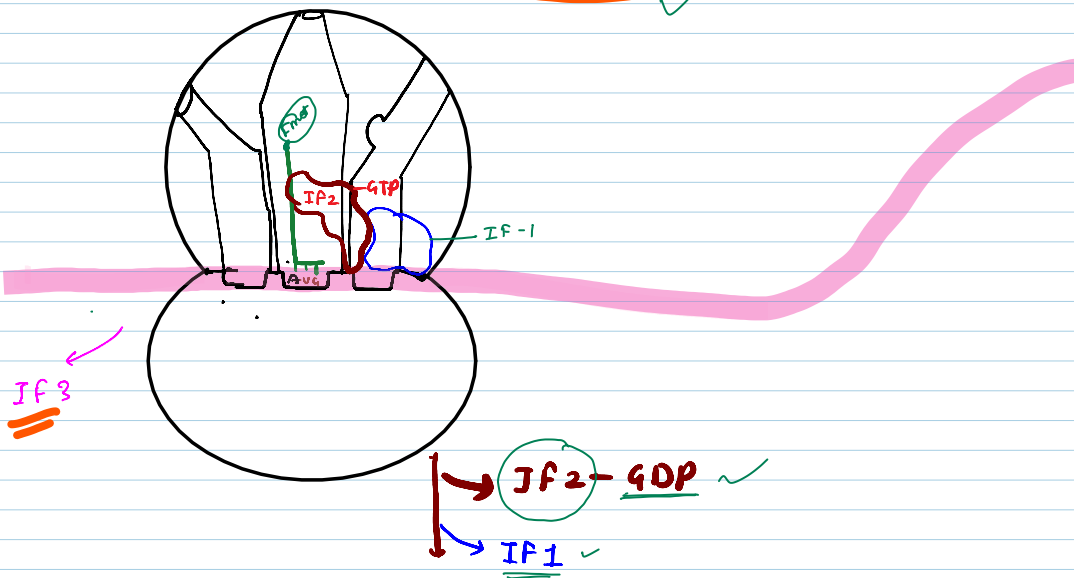
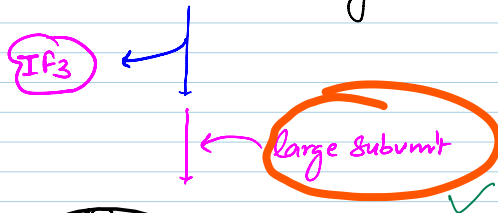


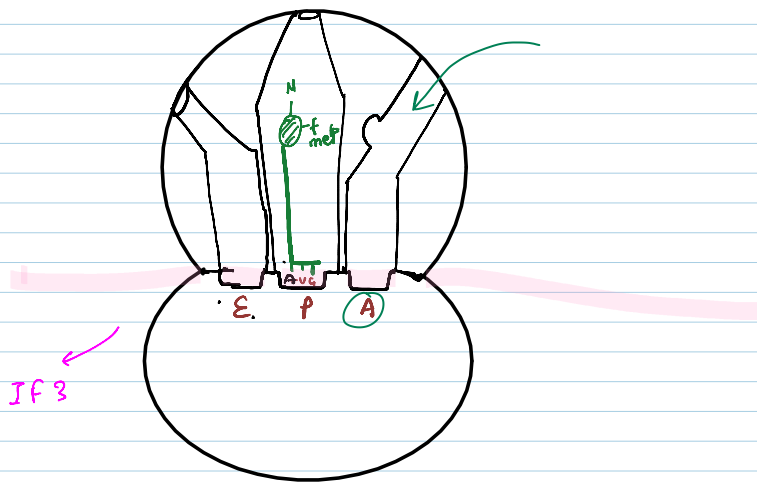


① Shine Dalgarno seq. Recognized by 16 S rRNA on Small Subunit of Ribosome

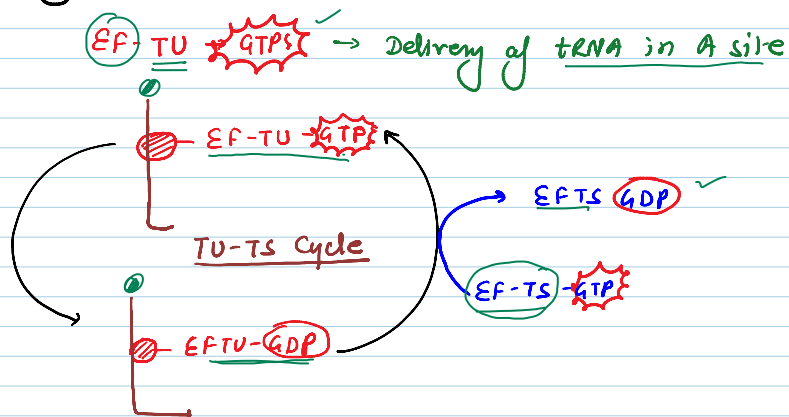
Initiator tRNA Recognized start codon ✓

Conformational change in Ribosome ✓



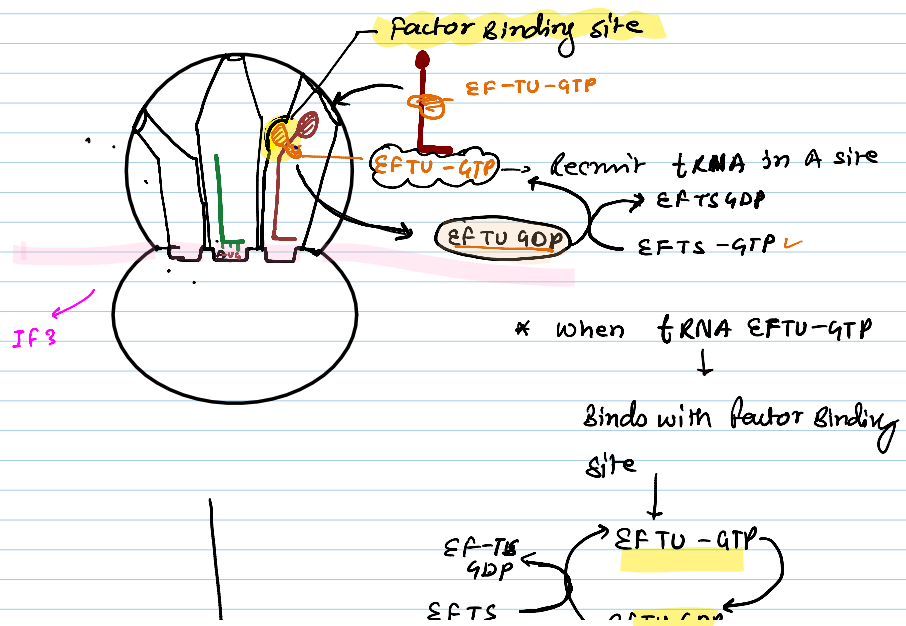


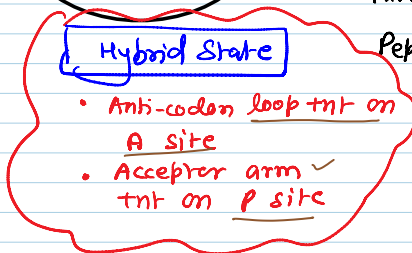
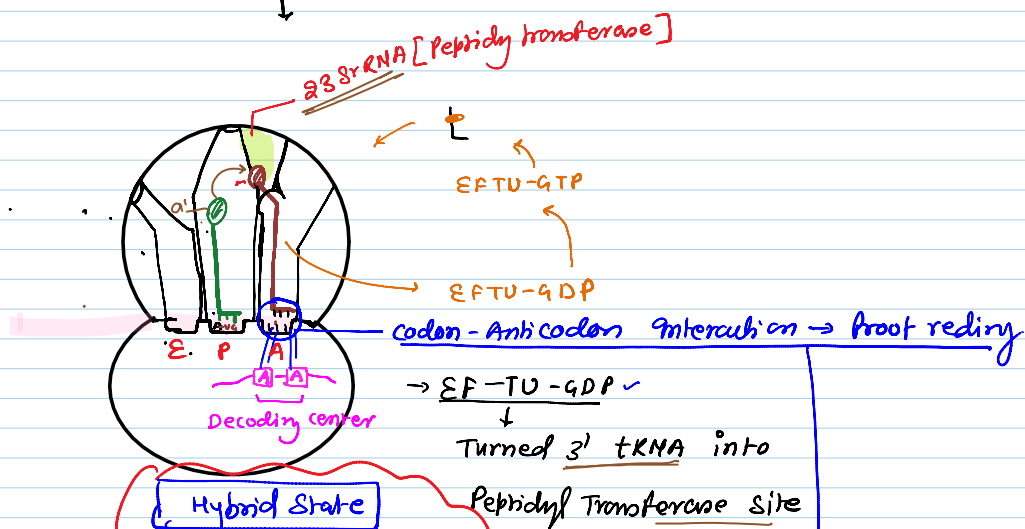
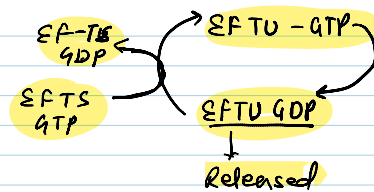
Elongation Step



Elongation Step

- (i) Delivery of tRNA in A site ✓
- (ii) Peptidyl Transferase (23-S- rRNA) - large subunit
- (iii) Translocase → [EF G] - GTP



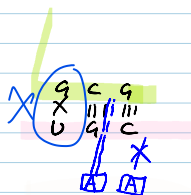
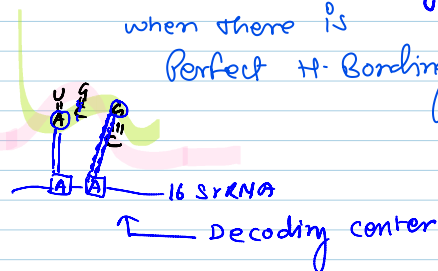


① Decoding Center

- AA of 16S rRNA near A site

- Intercalated with codon & anticodon for further stability

when there is Perfect H-Bonding.

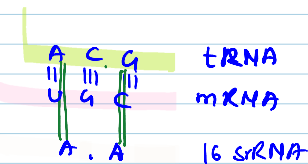


Decoding center

✓ [A] → Unstable Binding

Unstable in Hybrid state

✓ Incorrect tRNA Released



Correct tRNA

Stable interaction

Stable even in Hybrid state

Correct tRNA

✓ Peptidyl Transferase activity start

Transferase
activity starts

tRNA Accommodation -

- 3rd step of proof reading ✓

→ when EFTU GDP release from tRNA

tRNA → Hybrid State (Accommodation)

maintain if codon & anticodon
correct base pairing

if incorrect tRNA

Release of incorrect
tRNA

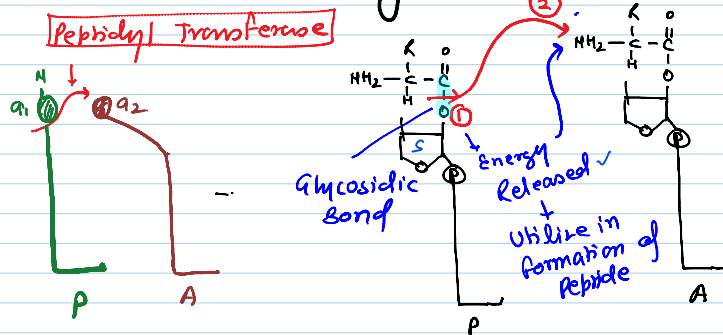
* Proof reading during translation -

✓ ① Charging of a.a. (tRNA Synthetase)

✓ ② Decoding center

✓ ③ Hybrid state (Accommodation)

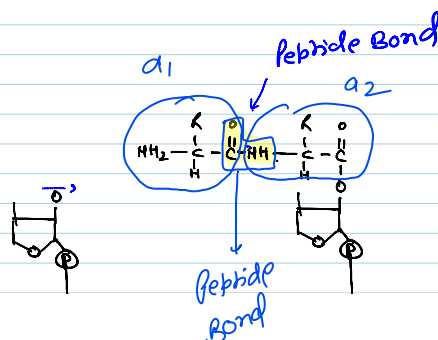
Peptidyl Transferase activity

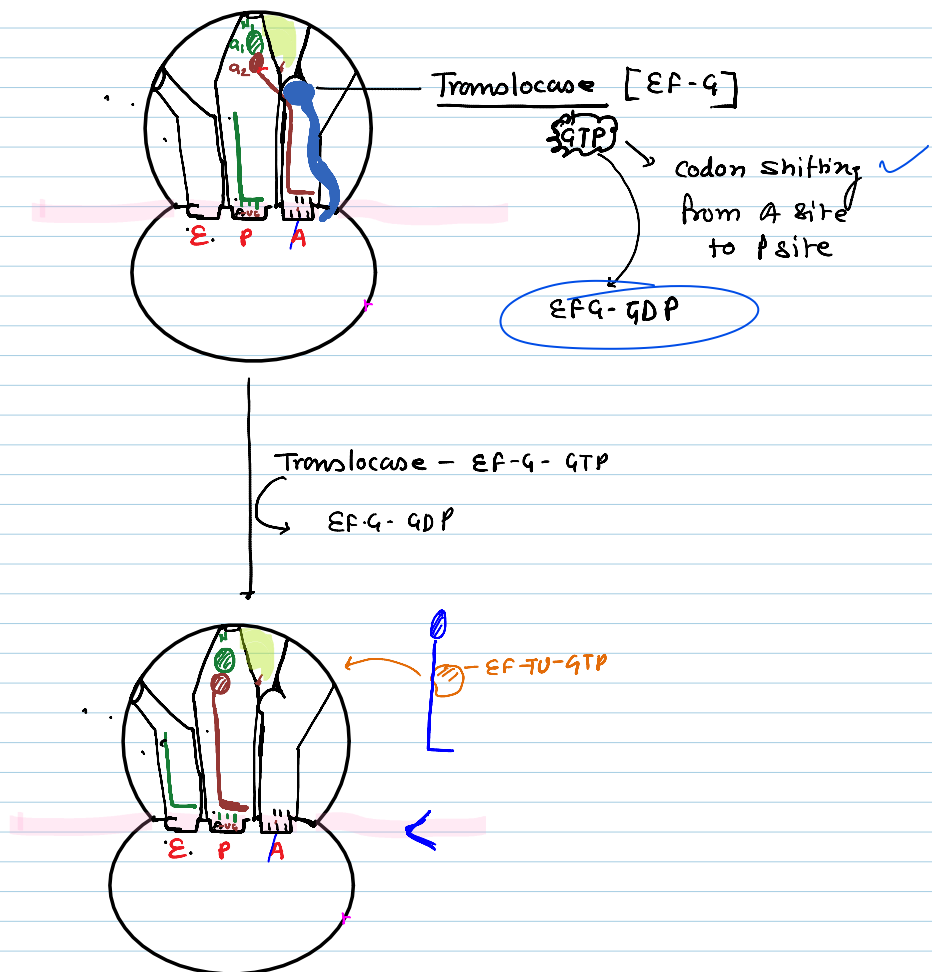
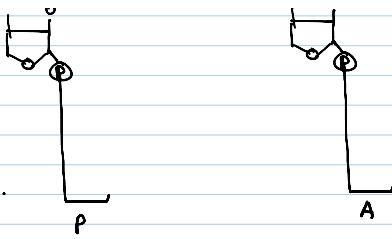


→ Peptidyl Transferase

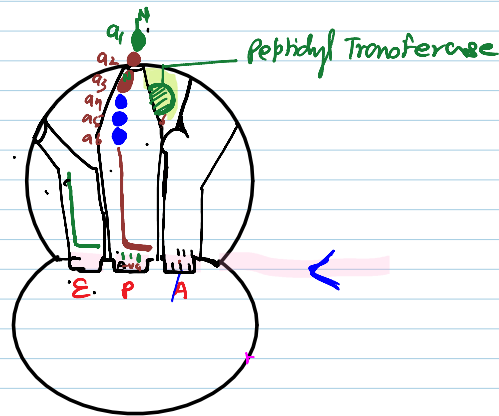
- 23 SrRNA - attack c ter. of Peptide / a.a. - ①
at P site tRNA

- Transfer a.a. on N-Ter. of New - (ii)
a.a. at A site

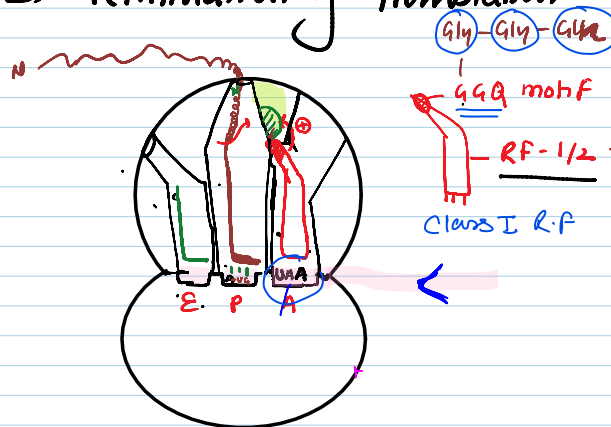




- # Total Energy Expenditure →
- for each a.a. → 1 ATP → tRNA loading (charging)
- 2 GTP
- 1-GTP → EF-TU
 - 1 GTP → Translocase activity



⇒ Termination of Translation



RF-1/2 → Enters in A site
 CLASS I R.F

Recognize Stop codon (UAA)
 GAG motif activate
 Peptidyl transferase activity
 Peptide transferred on water mole
 Peptide chain released

